

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 16, 2003, 13:59:32 ; Search time 39 Seconds
(Without alignments)
54.230 Million cell updates/sec

Title: US-09-914-213-2

Perfect score: 116

Sequence: 1 GLEISEINEDEKCFPDME 22

Scoring table: BIOSUM62

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR-73:*
2: PIR1:*
3: PIR2:*
4: PIR3:*
5: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	116	100.0	1480	1 DVHUCF	cystic fibrosis tr
2	106	91.4	1481	1 A39323	cystic fibrosis tr
3	103	88.8	1450	2 JC6139	cystic fibrosis tr
4	94	81.0	1485	2 S23756	CFTR protein - Afr
5	87	75.0	1476	1 A39901	cystic fibrosis tr
6	87	75.0	1476	1 A40303	cystic fibrosis tr
7	87	75.0	1492	2 A39322	cystic fibrosis tr
8	57	49.1	378	2 A32916	long-chain-fatty-a
9	51	44.0	705	2 H89900	translation initia
10	50	43.1	631	2 S67268	hypothetical prote
11	49	42.2	257	2 A28664	enterotoxin A prec
12	49	42.2	257	2 A28179	enterotoxin E prec
13	49	42.2	457	2 A64603	coproporphyrinogen
14	48.5	41.8	565	2 C69835	phosphomannomutase
15	48	41.4	154	2 G85041	probable calmoduli
16	48	41.4	154	2 G85041	coenzyme F420-quin
17	48	41.4	457	2 H71911	oxygen-independent
18	48	41.4	1087	2 T30330	gelosolin-related p
19	47.5	40.9	230	2 T28262	ORF MSV100 probabl
20	47	40.5	603	2 S76959	GTP-binding membra
21	47	40.5	1048	2 C86189	protein T25N20.11
22	46.5	40.1	235	1 E69883	phage-related repl
23	46.5	40.1	235	2 D84643	probable ATP-depen
24	46.5	40.1	360	2 T17423	probable acyl-CoA
25	46	39.7	104	2 D86830	thioredoxin (import
26	46	39.7	232	2 C89938	conserved hypotet
27	46	39.7	244	2 C96796	probable heat choc
28	46	39.7	373	2 S15161	long-chain-fatty-a
29	46	39.7	468	1 H64313	corrinoid/Iron-sul

30	46	39.7	515	2 C71158	probable thermosta
31	46	39.7	562	2 H88071	protein ZK1240.3
32	46	39.7	599	2 G83821	DNA primase dnag
33	46	39.7	707	1 DNMS	nucleolin - mouse
34	46	39.7	1336	2 T23310	hypothetical prote
35	46	39.7	1882	1 GNVVTR	genome polypeptide
36	45.5	39.2	1308	2 E71622	probable membrane
37	45	38.8	104	2 B69794	hypothetical prote
38	45	38.8	216	2 C88576	120G5.12 protein -
39	45	38.8	260	2 C70115	ribosomal protein
40	45	38.8	366	2 F71481	probable rod shape
41	45	38.8	366	2 D72027	cell shape-determi
42	45	38.8	366	2 H86596	rod shape protein
43	45	38.8	366	2 E81742	cell shape-determi
44	45	38.8	593	2 E81742	Na+-transporting A
45	45	38.8	953	2 AH1972	hypothetical prote

ALIGNMENTS

RESULT 1
DVHUCF
cystic fibrosis transmembrane conductance regulator - human
C:Species: Homo sapiens (man)
C:Date: 31-Dec-1990 #sequence_revision 28-Oct-1994 #text_change 16-Jul-1999
C:Accession: A39069; A30300; A42805; S10943; S15354; S10951
R:Zielenski, J.; Rozmahel, R.; Bozon, D.; Kerem, B.; Grzelczak, Z.; Riordan, J.R.; Ro
Genomics 10, 214-228, 1991
A:Title: Genomic DNA sequence of the cystic fibrosis transmembrane conductance regula
A:Reference number: A39069; MUID:91257831; PMID:1710598
A:Accession: A39069
A:Molecule type: DNA
A:Residues: 1-1480 <ZIE>
A:Cross-references: GB:M55131; NID:9306536; PIDN:AAC13657.1; PID:9306538
R:Riordan, J.R.; Rommens, J.M.; Kerem, B.; Alon, N.; Rozmahel, R.; Grzelczak, Z.; Zie
Science 245, 1066-1073, 1999
A:Title: Identification of the cystic fibrosis gene: cloning and characterization of
A:Reference number: A30300; MUID:89368940; PMID:2475911
A:Accession: A30300
A:Molecule type: mRNA
A:Residues: 1-619, 'N', 621-832, 'L', 834-1149, 'I', 1151-1480 <RIO>
A:Cross-references: GB:M28668; NID:9180331
A:Note: this sequence has been revised in reference A39069
A:Note: 75-Gln and 470-Val were also found
R:Ricciotto, M.R.; Conn, J.A.; Bertuzzi, G.; Greengard, P.; Nairn, A.C.
J. Biol. Chem. 267, 12742-12752, 1992
A:Title: Phosphorylation of the cystic fibrosis transmembrane conductance regulator.
A:Reference number: A42805; MUID:92316961; PMID:1377674
A:Accession: A42805
A:Molecule type: protein
A:Residues: 682-690, 'E', 693-725, 727-743, 747-815 <RIC>
R:Cutting, G.R.; Kasch, L.M.; Rosensteel, B.J.; Zielenski, J.; Tsui, L.C.; Antonarak
Nature 346, 366-369, 1990
A:Title: A cluster of cystic fibrosis mutations in the first nucleotide-binding fold
A:Reference number: S10943; MUID:90326187; PMID:1695717
A:Accession: S10943
A:Molecule type: nucleic acid sequence not shown
A:Status: nucleic acid sequence not shown
A:Residues: 542-560; 1340-1358 <CUT>
A:Note: Four mutations between residues 549-559 were identified in CF patients
R:Toshimura, K.; Nakamura, H.; Trapnell, B.C.; Dalemans, W.; Pavlenti, A.; Lecocq, J.
J. Biol. Chem. 266, 9140-9144, 1991
A:Title: The cystic fibrosis gene has a 'housekeeping'-type promoter and is expressed
A:Reference number: I55354; MUID:91225019; PMID:1709163
A:Accession: I55354
A:Molecule type: DNA
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-17 <RES>
A:Cross-references: GB:M58478; NID:9180291; PIDN:AAA1992.1; PID:9180292
A:Note: neither the complete nucleic acid sequence nor the complete translation are s
C:Comment: This protein (CFTR) is directly responsible for cystic fibrosis (CF), a di
piratory tract. A single residue deletion (Phe-508) is detected in most CF patients;

uctance across the apical membrane of epithelial cells.

C:Genetics:
A:Gene: GDB:CFTR; CF
A:Cross-References: GDB:120584; OMIM:219700
A:Map position: 7q31.2-7q31.2
A:Introns: 18/2: 55/2: 91/3: 163/3: 193/3: 248/2: 290/2: 372/3: 403/3: 464/3: 528/3: 560
C:Superfamily: cystic fibrosis transmembrane conductance regulator; ATP-binding cassette
C:Keywords: ATP; duplication; glycoprotein; nucleotide binding; P-loop; phosphoprotein;
F:118-102/Domain: transmembrane #status predicted <TM1>
F:118-138/Domain: transmembrane #status predicted <TM2>
F:195-215/Domain: transmembrane #status predicted <TM3>
F:221-241/Domain: transmembrane #status predicted <TM4>
F:308-328/Domain: transmembrane #status predicted <TM5>
F:331-350/Domain: transmembrane #status predicted <TM6>
F:441-622/Domain: ATP-binding cassette homology <ABC1>
F:458-465/Region: nucleotide-binding motif A (P-loop)
F:568-572/Region: nucleotide-binding motif B
F:590-830/Region: R domain
F:860-880/Domain: transmembrane #status predicted <TM7>
F:912-932/Domain: transmembrane #status predicted <TM8>
F:991-1011/Domain: transmembrane #status predicted <TM9>
F:1103-1123/Domain: transmembrane #status predicted <TM10>
F:1123-1150/Domain: transmembrane #status predicted <TM11>
F:1227-1419/Domain: ATP-binding cassette homology <ABC2>
F:1244-1251/Region: nucleotide-binding motif A (P-loop)
F:1366-1370/Region: nucleotide-binding motif B
F:464/Binding site: ATP (Lys) #status predicted
F:660/700/737,813/Binding site: phosphate (Ser) (covalent) (by cAMP- and cGMP-dependent
F:686/790/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status expected
F:768/795/Binding site: phosphate (Ser) (covalent) (by cAMP- and cGMP-dependent kinases)
F:894/900/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:1250/Binding site: ATP (Lys) #status predicted

Query Match 100.0%; Score 116; DB 1; Length 1480;
Best Local Similarity 100.0%; Pred. No. 8e-08;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLEISEINEEDLKECFDDME 22
DB 817 GLEISEINEEDLKECFDDME 838

RESULT 2
A39323

Cystic fibrosis transmembrane conductance regulator - bovine

C:Species: Bos primigenius taurus (cattle)

C>Date: 19-Jun-1992 #sequence_revision 28-Oct-1994 #text_change 16-Jul-1999

C:Accession: A39323

R:Diamond: G.; Scanlin, T.F.; Zaslloff, M.A.; Bevins, C.L.

J. Biol. Chem. 266, 22761-22769, 1991

A:Title: A cross-species analysis of the cystic fibrosis transmembrane conductance regul

A:Reference number: A39323; PMID:92042228; PMID:1719001

A:Accession: A39323

A:Molecule type: mRNA

A:Residues: 1-1481 <DIA>

A:Cross-References: GB:M76128; NID:g163741; PIDN:AAA30772.1; PID:g163742

A:Note: the authors translated the codon GGA for residue 725 as Phe and AGA for residue

C:Superfamily: cystic fibrosis transmembrane conductance regulator; ATP-binding cassette

C:Keywords: ATP; duplication; glycoprotein; nucleotide binding; P-loop; phosphoprotein;

F:81-102/Domain: transmembrane #status predicted <TM1>

F:118-138/Domain: transmembrane #status predicted <TM2>

F:195-215/Domain: transmembrane #status predicted <TM3>

F:221-241/Domain: transmembrane #status predicted <TM4>

F:308-328/Domain: transmembrane #status predicted <TM5>

F:331-350/Domain: transmembrane #status predicted <TM6>

F:440-621/Domain: ATP-binding cassette homology <ABC1>

F:457-464/Region: nucleotide-binding motif A (P-loop)

F:567-571/Region: nucleotide-binding motif B

F:589-830/Region: R domain

F:860-880/Domain: transmembrane #status predicted <TM7>

F:912-932/Domain: transmembrane #status predicted <TM8>

F:991-1011/Domain: transmembrane #status predicted <TM9>

F:1103-1123/Domain: transmembrane #status predicted <TM10>

F:1129-1150/Domain: transmembrane #status predicted <TM11>

F:1228-1420/Domain: ATP-binding cassette homology <ABC2>

F:1245-1252/Region: nucleotide-binding motif A (P-loop)

F:1367-1371/Region: nucleotide-binding motif B

F:463/Binding site: ATP (Lys) #status predicted

F:659/699/736,813/Binding site: phosphate (Ser) (covalent) (by cAMP- and cGMP-depende

F:685/790/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status expe

F:767/795/Binding site: phosphate (Ser) (covalent) (by cAMP- and cGMP-dependent kinas

F:894/900/Binding site: carbohydrate (Asn) (covalent) #status predicted

F:1251/Binding site: ATP (Lys) #status predicted

Query Match 91.4%; Score 106; DB 1; Length 1481;
Best Local Similarity 86.4%; Pred. No. 1.9e-06;
Matches 19; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLEISEINEEDLKECFDDME 22
DB 817 GLEISEINEEDLKECFDDME 838

RESULT 3
JC6139

Cystic fibrosis transmembrane conductance regulator - rabbit

C:Species: Oryctolagus cuniculus (domestic rabbit)

C>Date: 11-Apr-1997 #sequence_revision 09-May-1997 #text_change 28-May-1999

C:Accession: JC6139; E39323

R:Hart, P.; March, J.D.; Levesque, P.C.; Collier, M.L.; Geary, Y.; Horowitz, B.; Hume

Proc. Natl. Acad. Sci. U.S.A. 93, 6343-6348, 1996

A:Title: Cystic fibrosis gene encodes a cAMP-dependent chloride channel in heart.

A:Reference number: JC6139; PMID:96270540; PMID:8692817

A:Accession: JC6139

A>Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-1450 <HAR>

A:Cross-References: GB:U40227

R:Diamond: G.; Scanlin, T.F.; Zaslloff, M.A.; Bevins, C.L.

J. Biol. Chem. 266, 22761-22769, 1991

A:Title: A cross-species analysis of the cystic fibrosis transmembrane conductance re

A:Reference number: A39323; PMID:92042228; PMID:1719001

A:Accession: E39323

A>Status: preliminary; nucleic acid sequence not shown; not compared with conceptual

A:Molecule type: DNA

A:Residues: 574-604, 'N', 606-646, 'I', 648-684, 'P', 686-700, 'S', 702-718, 'V', 720-746 <DIA>

A:Comment: This regulator plays a role in defecting intracellular processing.

C:Genetics:

A:Gene: cfr

C:Superfamily: cystic fibrosis transmembrane conductance regulator; ATP-binding casse

C:Keywords: ATP; duplication; glycoprotein; nucleotide binding; P-loop; transmembrane

F:411-592/Domain: ATP-binding cassette homology <ABC1>

F:428-435/Region: nucleotide-binding motif A (P-loop)

F:1197-1389/Domain: ATP-binding cassette homology <ABC2>

F:1214-1221/Region: nucleotide-binding motif A (P-loop)

Query Match 88.8%; Score 103; DB 2; Length 1450;
Best Local Similarity 86.4%; Pred. No. 4e-06;
Matches 19; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GLEISEINEEDLKECFDDME 22
DB 787 GLEISEINEEDLKECFDDME 808

RESULT 4
S23756

CFTR protein - African clawed frog

C:Species: Xenopus laevis (African clawed frog)

C>Date: 05-Mar-1994 #sequence_revision 01-Sep-1995 #text_change 02-Feb-2001

C:Accession: S23756

R:Trucker, S.J.; Tannahill, D.; Higgins, C.F.

Hum. Mol. Genet. 1, 77-82, 1992

A:Title: Identification and developmental expression of the Xenopus laevis cystic fib

A:Reference number: S23756; PMID:93244789; PMID:1284470

A:Accession: S23756

A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1485 <TUC>
A:Cross-references: EMBL:X65256; NID:g64622; PIDN:CAA46348.1; PID:g64623
C:Superfamily: cystic fibrosis transmembrane conductance regulator; ATP-binding cassette
C:Keywords: ATP; nucleotide binding; P-loop; transmembrane protein
F:442-623/Domain: ATP-binding cassette homology <ABC1>
F:459-466/Region: nucleotide-binding motif A (P-loop)
F:1230-1422/Domain: ATP-binding cassette homology <ABC2>
F:1247-1254/Region: nucleotide-binding motif A (P-loop)

Query Match 81.0%; Score 94; DB 2; Length 1485;
Best Local Similarity 81.0%; Pred. No. 8; 6e-05;

Matches 17; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 2 LEISEINEEDLKECFDDME 22
Db 820 LEVSEINEEDLKECFDDTD 840

RESULT 5

Cystic fibrosis transmembrane conductance regulator - mouse (strain C57/BL/6J)
C:Species: Mus musculus domesticus (western European house mouse)
C:Date: 20-Mar-1992 #sequence_revision 28-Oct-1994 #text_change 16-Jul-1999

C:Accession: A39901; A42007

R:Title: Cloning the mouse homolog of the human cystic fibrosis transmembrane conductance

A:Reference number: A39901; MUID:9130183; PMID:1712752

A:Accession: A39901

A:Molecule type: mRNA

A:Residues: 1-1476 <TAT>

A:Cross-references: GB:M69298; NID:g192566; PIDN:AAA37417.1; PID:g192567

R:Title: Expression and chromosome localization of the murine cystic fibrosis transmembrane

A:Reference number: A42007; MUID:92307673; PMID:1377165

A:Accession: A42007

A:Molecule type: DNA

A:Residues: 465-528 <KEL>

A:Cross-references: GB:M64614

C:Genetics:

A:Gene: CFTR

A:Map position: 6

C:Superfamily: cystic fibrosis transmembrane conductance regulator; ATP-binding cassette
C:Keywords: ATP; duplication; glycoprotein; nucleotide binding; P-loop; phosphoprotein;

F:81-102/Domain: transmembrane #status predicted <TM1>

F:118-138/Domain: transmembrane #status predicted <TM2>

F:195-215/Domain: transmembrane #status predicted <TM3>

F:221-241/Domain: transmembrane #status predicted <TM4>

F:308-338/Domain: transmembrane #status predicted <TM5>

F:331-350/Domain: transmembrane #status predicted <TM6>

F:441-622/Domain: ATP-binding cassette homology <ABC1>

F:458-465/Region: nucleotide-binding motif A (P-loop)

F:568-572/Region: nucleotide-binding motif B

F:590-825/Region: R domain

F:855-875/Domain: transmembrane #status predicted <TM7>

F:907-927/Domain: transmembrane #status predicted <TM8>

F:986-1006/Domain: transmembrane #status predicted <TM9>

F:1098-1118/Domain: transmembrane #status predicted <TM10>

F:1124-1145/Domain: transmembrane #status predicted <TM11>

F:1223-1415/Domain: ATP-binding cassette homology <ABC2>

F:1240-1247/Region: nucleotide-binding motif A (P-loop)

F:1362-1366/Region: nucleotide-binding motif B

F:464/Binding site: ATP (Lys) #status predicted

F:660-698-732-808/Binding site: phosphate (Ser) (covalent) (by cAMP- and cGMP-dependent

F:684-785/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status experim

F:763-790/Binding site: phosphate (Ser) (covalent) (by cAMP- and cGMP-dependent kinases)

F:889-895/Binding site: carboxylate (Asn) (covalent) #status predicted

F:1246/Binding site: ATP (Lys) #status predicted

Query Match 75.0%; Score 87; DB 1; Length 1476;

Best Local Similarity 80.0%; Pred. No. 0.00079;
Matches 16; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 2 LEISEINEEDLKECFDDM 21
Db 813 LNTIEINEEDLKECFDDV 832

RESULT 6

A40303

Cystic fibrosis transmembrane conductance regulator - mouse

C:Species: Mus musculus (house mouse)

C:Date: 03-Apr-1992 #sequence_revision 28-Oct-1994 #text_change 16-Jul-1999

C:Accession: A40303; I78528

R:Title: Molecular cloning and sequence analysis of the murine cDNA for the cystic fi

A:Reference number: A40303; MUID:91365359; PMID:1716243

A:Accession: A40303

A:Molecule type: mRNA

A:Residues: 1-1476 <YOR>

A:Cross-references: GB:M60493; NID:g192831; PIDN:AA18903.1; PID:g192832

A:Experimental source: lung; strain BALB/cBy

R:Delaney, S.J.; Rich, D.P.; Thomson, S.A.; Hargrave, M.R.; Lovelock, P.K.; Welsh, M.

Nature Genet. 4, 426-431, 1993

A:Title: Cystic fibrosis transmembrane conductance regulator splice variants are not

A:Reference number: I58115; MUID:94004974; PMID:7691356

A:Accession: I78528

A:Status: translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 549-571 <RES>

A:Cross-references: GB:S65942; NID:g430810; PIDN:AAB28391.1; PID:g430811

C:Genetics:

A:Gene: CFTR

A:Map position: 6

A:Introns: 560/2

A>Note: the list of introns is incomplete

C:Superfamily: cystic fibrosis transmembrane conductance regulator; ATP-binding case

C:Keywords: ATP; duplication; glycoprotein; nucleotide binding; P-loop; phosphoprotein

F:81-102/Domain: transmembrane #status predicted <TM1>

F:118-138/Domain: transmembrane #status predicted <TM2>

F:195-215/Domain: transmembrane #status predicted <TM3>

F:221-241/Domain: transmembrane #status predicted <TM4>

F:308-328/Domain: transmembrane #status predicted <TM5>

F:331-350/Domain: transmembrane #status predicted <TM6>

F:441-622/Domain: ATP-binding cassette homology <ABC1>

F:458-465/Region: nucleotide-binding motif A (P-loop)

F:568-572/Region: nucleotide-binding motif B

F:590-825/Region: R domain

F:855-875/Domain: transmembrane #status predicted <TM7>

F:907-927/Domain: transmembrane #status predicted <TM8>

F:986-1006/Domain: transmembrane #status predicted <TM9>

F:1098-1118/Domain: transmembrane #status predicted <TM10>

F:1124-1145/Domain: transmembrane #status predicted <TM11>

F:1223-1415/Domain: ATP-binding cassette homology <ABC2>

F:1240-1247/Region: nucleotide-binding motif A (P-loop)

F:1362-1366/Region: nucleotide-binding motif B

F:464/Binding site: ATP (Lys) #status predicted

F:660-698-732-808/Binding site: phosphate (Ser) (covalent) (by cAMP- and cGMP-depende

F:684-785/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status exper

F:763-790/Binding site: phosphate (Ser) (covalent) (by cAMP- and cGMP-dependent kins

F:889-895/Binding site: carboxylate (Asn) (covalent) #status predicted

F:1246/Binding site: ATP (Lys) #status predicted

Query Match 75.0%; Score 87; DB 1; Length 1476;

Best Local Similarity 80.0%; Pred. No. 0.00079;

Matches 16; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 2 LEISEINEEDLKECFDDM 21
Db 813 LNTIEINEEDLKECFDDV 832

Probable calmodulin [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 23-Mar-2001
C:Accession: G85041
R:anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Spring
Nature 402, 769-777, 1999
A:title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
A:Reference number: A85001; MUID:20083488; PMID:10617198
A:Accession: G85041
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1154 <STO>
A:Cross-references: GB:NC_001268; NID:97270199; PIDN:CAB77814.1; GSPDB:GN00140
C:Genetics:
A:Gene: AT4g03290
A:Map position: 4
C:superfamily: calmodulin; calmodulin repeat homology
C:keywords: EF hand

Query Match 41.4%; Score 48; DB 2; Length 154;
Best Local Similarity 50.0%; Pred. No. 18;
Matches 10; Conservative 4; Mismatches 4; Indels 2; Gaps 1;
QY 2 LEISEINEEDLKECF--FD 19
:|:|:|:|:|:|:|:|:|
Db 71 VEDEDEVGEEDMKFAFNVPD 90

Search completed: July 16, 2003, 14:03:53
Job time : 41 secs